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| 09/341,641 | 09/09/1999 | GUNTER SCHMIDT | 020600-280 | 5378 |

21839 7590 12/04/2003

BURNS DOANE SWECKER & MATHIS L L P
POST OFFICE BOX 1404
ALEXANDRIA, VA 22313-1404

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| EXAMINER |
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CHAKRABARTI, ARUN K

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| ART UNIT | PAPER NUMBER |
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1634

DATE MAILED: 12/04/2003

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.
09/341,641

Applicant(s)
Schmidt et al.

Examiner
Arun Chakrabarti

Art Unit
1634



-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

- 1) ☒ Responsive to communication(s) filed on Nov 5, 2003
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11; 453 O.G. 213.

Disposition of Claims

- 4) ☒ Claim(s) 21-39 and 41-43 is/are pending in the application.
- 4a) Of the above, claim(s) _____ is/are withdrawn from consideration.
- 5) ☐ Claim(s) _____ is/are allowed.
- 6) ☒ Claim(s) 21-39 and 41-43 is/are rejected.
- 7) ☐ Claim(s) _____ is/are objected to.
- 8) ☐ Claims _____ are subject to restriction and/or election requirement.

Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on _____ is/are a) ☐ accepted or b) ☐ objected to by the Examiner.
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).
- 11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.
If approved, corrected drawings are required in reply to this Office action.
- 12) ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

- 13) ☐ Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
 - ☐ Certified copies of the priority documents have been received in Application No. _____.
 - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

*See the attached detailed Office action for a list of the certified copies not received.

- 14) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).
- a) ☐ The translation of the foreign language provisional application has been received.
- 15) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

- 1) ☒ Notice of References Cited (PTO-892) 4) ☐ Interview Summary (PTO-413) Paper No(s). _____
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948) 5) ☐ Notice of Informal Patent Application (PTO-152)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449) Paper No(s). _____ 6) ☒ Other: **Detailed Action**

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DETAILED ACTION

Continued Examination Under 37 CFR 1.114

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on November 5, 2003 has been entered.

Claim Rejections - 35 USC § 103

2. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was

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made in order for the examiner to consider the applicability of 35 U.S.C. 103© and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

3. Claims 21-32 are rejected under 35 U.S.C. 103(a) as being obvious over Southern et al. (PCT International Publication Number: WO 95/04160) (February 9, 1995) in view of Cantor (U.S. Patent 5,503,980) (April 2, 1996).

Southern et al. teaches a method for sequencing DNA (Abstract with Figure), which comprises:

(a) obtaining a target DNA population comprising a plurality of single-stranded DNAs to be sequenced, each of which is present in a unique amount in the same reaction zone and bears a primer to provide a double-stranded portion of the DNA for ligation thereto(Figure 5 and Example 16 b, lines 1-12 and Claims 16 a and 16 b);

(b) contacting the DNA population with an array of hybridization probes, each probe comprising a label cleavably attached to a known base sequence of predetermined length, the array containing all possible base sequences of that predetermined length and the base sequence being incapable of ligation to each other, wherein the contacting is carried out in the presence of ligase under conditions to ligate to the double-stranded portion of each DNA the probe bearing the base sequence complementary to the single-stranded DNA adjacent the double-stranded portion thereby to form an extended double-stranded portion which is incapable of ligation to further probes (Figures 4 and 5 and Claims 16 a to 16 d and Claims 20 a to 20 d);

c) removing all unligated probes (Claims 16 e and 20 e); followed by the steps of :

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(d) cleaving the ligated probes to release each label (Figures 3a, 3b and 4, and Page 16, lines 5-18 and Example 18);

(e) recording the quantity of each label (Example 19, Figures 3b, 4 and 5 and claims 16 f and 20 f); and

(f) activating the extended double-stranded portion to enable ligation thereto (Page 16, lines 15-18, Figures 4 and 5);

(g) steps (b) to (f) are repeated in a cycle for a sufficient number of times to determine the sequence of each single-stranded DNA by determining the sequence of release of each label (Figure 4 and page 16, lines 19-26 and claim 17).

Southern et al. teaches a method wherein the array comprises a plurality of sub-arrays which together contains all possible base sequences (Page 17, line 1 to page 18, line 5 and page 19, line 26 to page 21, lines 23 and claim 20).

Southern et al. teaches a method wherein the initial DNA sample is cut into fragments, each having a sticky end of known length and unknown sequence, which fragments are sorted into subpopulations according to their sticky end sequence (Example 16 b).

Southern et al. teaches a method wherein each single-stranded DNA is immobilized at one end (Figures 4 and 5).

Southern et al. teaches a method wherein the label of each probe comprises a mass label, and the quantity of each label is recorded using mass spectrometry after release of the label (Example 19).

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Southern et al. teaches a method wherein the known base sequence is blocked at its 3' OH (Figure 4, step 1).

Southern et al. teaches a method wherein the step of cleaving the ligated probes to release each label unblocks the 3' -OH of the extended double-stranded portion (Figure 4, step 2).

Southern et al. teaches a method wherein the label of each probe is cleavably attached to the 3'-OH of the base sequence (Figure 4).

Southern et al. teaches a method wherein the base sequence of each probe is unphosphorylated at both 3' and 5' ends and comprises phosphorylating the 5'-OH of the extended double-stranded position (Figure 4, steps 3 and 4).

Southern et al. teaches a method wherein the predetermined length of the base sequence is from 2 to 6 (Page 2, lines 2-8).

Southern et al does not teach a method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation.

Cantor teaches a method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation (Example 10 and claims 1-37).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation of Cantor into the sequencing by hybridization of Southern et al., since Cantor states, "Probes created herein may be used to quickly, easily, and accurately identify that mutation or variation

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without having to perform a single conventional sequencing reaction (Column 4, lines 3-6)".

Cantor further provides motivation as Cantor states, "Therefore, the customized probes greatly lend themselves to use in , for example, diagnostic aids for the genetic screening of a biological sample (Column 10, lines 26-29)". An ordinary practitioner would have been motivated to combine and substitute the method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation of Cantor into the sequencing by hybridization of Southern et al. in order to achieve the express advantages, as noted by Cantor, of a method which provides probes that may be used to quickly, easily, and accurately identify that mutation or variation without having to perform a single conventional sequencing reaction and which may be used in diagnostic aids for the genetic screening of a biological sample.

4. Claims 21-25 and 27-32 are rejected under 35 U.S.C. 103(a) as being obvious over Macevicz et al. (PCT International Publication Number: WO 96/33205) (October 24, 1996) in view of Cantor (U.S. Patent 5,503,980) (April 2, 1996).

Macevicz et al. teaches a method for sequencing DNA (Abstract with Figure), which comprises:

(a) obtaining a target DNA population comprising a plurality of single-stranded DNAs to be sequenced, each of which is present in a unique amount in the same reaction zone and bears a primer to provide a double-stranded portion of the DNA for ligation thereto(Figure 1 and page 10, lines 16 to page 11, lines 23);

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(b) contacting the DNA population with an array of hybridization probes, each probe comprising a label cleavably attached to a known base sequence of predetermined length, the array containing all possible base sequences of that predetermined length and the base sequence being incapable of ligation to each other, wherein the contacting is carried out in the presence of ligase under conditions to ligate to the double-stranded portion of each DNA the probe bearing the base sequence complementary to the single-stranded DNA adjacent the double-stranded portion thereby to form an extended double-stranded portion which is incapable of ligation to further probes (Figures 1-4 and Claim 13);

c) removing all unligated probes (Claim 13); followed by the steps of :

(d) cleaving the ligated probes to release each label (Figures 1-4);

(e) recording the quantity of each label (Example 1, page 21, lines 19-27); and

(f) activating the extended double-stranded portion to enable ligation thereto (Figures 1-4 and Example 1, page 21, last paragraph);

(g) steps (b) to (f) are repeated in a cycle for a sufficient number of times to determine the sequence of each single-stranded DNA by determining the sequence of release of each label (Figures 1-4 and Example 1, page 21, last paragraph).

Macevicz et al. teaches a method wherein the array comprises a plurality of sub-arrays which together contains all possible base sequences (Example 1).

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Macevicz et al. teaches a method wherein the initial DNA sample is cut into fragments, each having a sticky end of known length and unknown sequence, which fragments are sorted into subpopulations according to their sticky end sequence (page 5, line 25 to page 6, line 18).

Macevicz et al. teaches a method wherein each single-stranded DNA is immobilized at one end (Figures 1-4).

Macevicz et al. teaches a method wherein the known base sequence is blocked at its 3' OH (Figure 4, step 2).

Macevicz et al. teaches a method wherein the step of cleaving the ligated probes to release each label unblocks the 3' -OH of the extended double-stranded portion (Figure 4, step 3).

Macevicz et al. teaches a method wherein the label of each probe is cleavably attached to the 3'-OH of the base sequence (Figure 4, steps 4 and 5).

Macevicz et al. teaches a method wherein the base sequence of each probe is unphosphorylated at both 3' and 5' ends and comprises phosphorylating the 5'-OH of the extended double-stranded position (Figures 2 and 3b).

Macevicz et al. teaches a method wherein the predetermined length of the base sequence is from 2 to 6 (Page 7, lines 7-20).

Macevicz et al. does not teach a method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation.

Cantor teaches a method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation (Example 10 and claims 1-37).

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It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine and substitute the method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation of Cantor into the sequencing by hybridization of Macevitz et al., since Cantor states, “Probes created herein may be used to quickly, easily, and accurately identify that mutation or variation without having to perform a single conventional sequencing reaction (Column 4, lines 3-6)”. Cantor further provides motivation as Cantor states, “Therefore, the customized probes greatly lend themselves to use in , for example, diagnostic aids for the genetic screening of a biological sample (Column 10, lines 26-29)”. An ordinary practitioner would have been motivated to combine and substitute the method for sequencing a heterogeneous population of single stranded DNA molecules simultaneously and without spatial separation of Cantor into the sequencing by hybridization of Macevitz et al. in order to achieve the express advantages, as noted by Cantor, of a method which provides probes that may be used to quickly, easily, and accurately identify that mutation or variation without having to perform a single conventional sequencing reaction and which may be used in diagnostic aids for the genetic screening of a biological sample.

5. Claims 21-39 and 41-43 are rejected under 35 U.S.C. 103 (a) as being unpatentable over Southern et al. (PCT International Publication Number: WO 95/04160) (February 9, 1995) in view of Cantor (U.S. Patent 5,503,980) (April 2, 1996) further in view of Stratagene Catalog (1988, page 39).

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Southern et al. in view of Cantor teaches the method of claims of 21-32 including array of hybridization probes comprising mass labels as described above.

Southern et al. in view of Cantor do not teach the motivation to combine all the reagents for identifying a base at a target position in a single-stranded sample DNA sequence in the form of a kit.

Stratagene catalog teaches a motivation to combine reagents into kit format (page 39).

It would have been *prima facie* obvious to one having ordinary skill in the art at the time the invention was made to combine all the reagents e.g., array of hybridization probes comprising mass labels etc. into a kit format as discussed by Stratagene catalog since the Stratagene catalog teaches a motivation for combining reagents of use in an assay into a kit, "Each kit provides two services: 1) a variety of different reagents have been assembled and pre-mixed specifically for a defined set of experiments. Thus one need not purchase gram quantities of 10 different reagents, each of which is needed in only microgram amounts, when beginning a series of experiments. When one considers all of the unused chemicals that typically accumulate in weighing rooms, desiccators, and freezers, one quickly realizes that it is actually far more expensive for a small number of users to prepare most buffer solutions from the basic reagents. Stratagene provides only the quantities you will actually need, premixed and tested. In actuality, the kit format saves money and resources for everyone by dramatically reducing waste. 2) The other service provided in a kit is quality control". (page 39, column 1).

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Response to Arguments

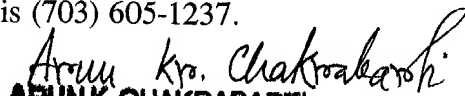
6. Applicant's arguments with respect to all pending claims have been considered but are moot in view of the new ground(s) of rejection.

Response to Amendment

7. In response to amendment, previous 102(b) rejections have been withdrawn. However, new 103(a) rejections have been included.

Conclusion


8. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Arun Chakrabarti, Ph.D., whose telephone number is (703) 306-5818. The examiner can normally be reached on 7:00 AM-4:30 PM from Monday to Friday. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion, can be reached on (703) 308-1119. The fax phone number for this Group is (703) 305-7401. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group LIE Chantae Dessau whose telephone number is (703) 605-1237.


ARUN K. CHAKRABARTI
PATENT EXAMINER

Arun Chakrabarti,

Patent Examiner,

November 17, 2003


GARY BENZION, PH.D.
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600